

0280

OIPPE

RAW SEQUENCE LISTING DATE: 09/26/2000  
PATENT APPLICATION: US/09/664,840 TIME: 12:02:24

Input Set : A:\BB1117 US NA Seq Listing.txt  
Output Set: N:\CRF3\09262000\I664840.raw

ENTERED

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61 Leu Arg Leu Ser Leu Tyr Phe Pro Ile Ser Ile Ser Leu Ser Leu Ser  
 62 1 5 10 15  
 64 Leu Glu Ala Met Ala Ser Phe Ile Ala Thr Thr Thr Pro Ala Met Pro  
 65 20 25 30  
 67 Ala Phe Ala Ser Val Leu Asp Pro Lys Ile Pro Thr Lys Pro Glu Pro  
 68 35 40 45  
 70 Lys Thr Glu Thr Pro Lys Pro Lys Asp Asp Leu Glu Arg Phe Arg Thr  
 71 50 55 60  
 73 Ser Glu Val Val Leu Glu Arg Lys Ser Lys Gly Phe Trp Arg Arg Lys  
 74 65 70 75 80  
 76 Trp Asn Pro Arg Asp Ile Gln Asn Ala Val Thr Leu Leu Val Leu His  
 77 85 90 95  
 79 Ala Leu Ala Ala Met Ala Pro Phe Tyr Phe Ser Trp Asp Ala Phe Trp  
 80 100 105 110  
 82 Ile Ser Phe Ile Leu Leu Gly Phe Ala Ser Gly Val Leu Gly Ile Thr  
 83 115 120 125  
 85 Leu Cys Phe His Arg Cys Leu Thr His Gly Gly Phe Lys Leu Pro Lys  
 86 130 135 140  
 88 Leu Val Glu Tyr Phe Phe Ala Tyr Cys Gly Ser Leu Ala Leu Gln Gly  
 89 145 150 155 160  
 91 Asp Pro Met Glu Trp Val Ser Asn His Arg Tyr His His Gln Phe Val  
 92 165 170 175  
 94 Asp Thr Glu Arg Asp Val His Ser Pro Thr Gln Gly Phe Trp Phe Cys  
 95 180 185 190  
 97 His Ile Gly Trp Val Leu Asp Lys Asp Leu Phe Val Glu Lys Arg Gly  
 98 195 200 205  
 100 Gly Arg Arg Asn Asn Val Asn Asp Leu Lys Lys Gln Ala Phe Tyr Arg  
 101 210 215 220  
 103 Phe Leu Gln Lys Thr Tyr Met Tyr His Gln Leu Ala Leu Ile Ala Leu  
 104 225 230 235 240  
 106 Leu Tyr Tyr Val Gly Gly Phe Pro Tyr Ile Val Trp Gly Met Gly Phe  
 107 245 250 255  
 109 Arg Leu Val Phe Met Phe His Ser Thr Phe Ala Ile Asn Ser Val Cys  
 110 260 265 270  
 112 His Lys Trp Gly Gly Arg Pro Trp Asn Thr Gly Asp Leu Ser Thr Asn  
 113 275 280 285  
 115 Asn Met Phe Val Ala Leu Cys Ala Phe Gly Glu Gly Trp His Asn Asn  
 116 290 295 300  
 118 His His Ala Phe Glu Gln Ser Ala Arg His Gly Leu Glu Trp Trp Gln  
 119 305 310 315 320  
 121 Ile Asp Val Thr Trp Tyr Val Ile Arg Thr Leu Gln Ala Ile Gly Leu  
 122 325 330 335  
 124 Ala Thr Asn Val Lys Leu Pro Thr Glu Ala Gln Lys Gln Lys Leu Lys  
 125 340 345 350  
 127 Ala Lys Ser Ala  
 128 355  
 130 <210> SEQ ID NO: 3  
 131 <211> LENGTH: 305  
 132 <212> TYPE: PRT

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133 <213> ORGANISM: Arabidopsis thaliana  
 135 <400> SEQUENCE: 3  
 136 Met Ser Leu Ser Ala Ser Glu Lys Glu Glu Asn Asn Lys Lys Met Ala  
 137 1 5 10 15  
 139 Ala Asp Lys Ala Glu Met Gly Arg Lys Lys Arg Ala Met Trp Glu Arg  
 140 20 25 30  
 142 Lys Trp Lys Arg Leu Asp Ile Val Lys Ala Phe Ala Ser Leu Phe Val  
 143 35 40 45  
 145 His Phe Leu Cys Leu Leu Ala Pro Phe Asn Phe Thr Trp Pro Ala Leu  
 146 50 55 60  
 148 Arg Val Ala Leu Ile Val Tyr Thr Val Gly Gly Leu Gly Ile Thr Val  
 149 65 70 75 80  
 151 Ser Tyr His Arg Asn Leu Ala His Arg Ser Phe Lys Val Pro Lys Trp  
 152 85 90 95  
 154 Leu Glu Tyr Phe Phe Ala Tyr Cys Gly Leu Leu Ala Ile Gln Gly Asp  
 155 100 105 110  
 157 Pro Ile Asp Trp Val Ser Thr His Arg Tyr His His Gln Phe Thr Asp  
 158 115 120 125  
 160 Ser Asp Arg Asp Pro His Ser Pro Asn Glu Gly Phe Trp Phe Ser His  
 161 130 135 140  
 163 Leu Leu Trp Leu Phe Asp Thr Gly Tyr Leu Val Glu Lys Cys Gly Arg  
 164 145 150 155 160  
 166 Arg Thr Asn Val Glu Asp Leu Lys Arg Gln Trp Tyr Tyr Lys Phe Leu  
 167 165 170 175  
 169 Gln Arg Thr Val Leu Tyr His Ile Leu Thr Phe Gly Phe Leu Leu Tyr  
 170 180 185 190  
 172 Tyr Phe Gly Gly Leu Ser Phe Leu Thr Trp Gly Met Gly Ile Gly Val  
 173 195 200 205  
 175 Ala Met Glu His His Val Thr Cys Leu Ile Asn Ser Leu Cys His Val  
 176 210 215 220  
 178 Trp Gly Ser Arg Thr Trp Lys Thr Asn Asp Thr Ser Arg Asn Val Trp  
 179 225 230 235 240  
 181 Trp Leu Ser Val Phe Ser Phe Gly Glu Ser Trp His Asn Asn His His  
 182 245 250 255  
 184 Ala Phe Glu Ser Ser Ala Arg Gln Gly Leu Glu Trp Trp Gln Ile Asp  
 185 260 265 270  
 187 Ile Ser Trp Tyr Ile Val Arg Phe Leu Glu Ile Ile Gly Leu Ala Thr  
 188 275 280 285  
 190 Asp Val Lys Leu Pro Ser Glu Ser Gln Arg Arg Arg Met Ala Met Val  
 191 290 295 300  
 193 Arg  
 194 305  
 196 <210> SEQ ID NO: 4  
 197 <211> LENGTH: 1807  
 198 <212> TYPE: DNA  
 199 <213> ORGANISM: Limnanthes douglasii  
 201 <220> FEATURE:  
 202 <221> NAME/KEY: unsure  
 203 <222> LOCATION: (302)..(303)

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205 <220> FEATURE:  
 206 <221> NAME/KEY: unsure  
 207 <222> LOCATION: (312) /  
 209 <220> FEATURE:  
 210 <221> NAME/KEY: unsure  
 211 <222> LOCATION: (315) /  
 213 <220> FEATURE:  
 214 <221> NAME/KEY: unsure  
 215 <222> LOCATION: (421) /  
 217 <220> FEATURE:  
 218 <221> NAME/KEY: unsure  
 219 <222> LOCATION: (1727) /  
 221 <400> SEQUENCE: 4

222 ctcactctca caccccttc tctctctttg tcgggttctc cggcgagata ctaaacggat 60  
 223 tcaatcgaag ggtgttacaa tatgtcgag acaaaacctg agaaacctt gatcgaacc 120  
 224 gtggaaaaca cactaccgtt tttaaaacta tcaataacta taaaacacgt gaaactcggt 180  
 225 taccattacc tgatcacca tggaaatgtac ctgtgtctcc ctctctcgc actagtctc 240  
 226 ttgcgtcaaa tctcaactt gtcctcaaa gatttcaacg acatctggaa acagcttcag 300  
 W--> 227 tnnatctca tntcngtctg tgtttcatca acacttcttg tctcttact tattcctttac 360  
 W--> 228 ttccatgactc gtcccgaggcc gggttatttg atggatttcg cgtgtcttata acccgacgaa 420  
 W--> 229 ntcgaaaat ctactagaga acatttttatg aagtgtggtg agagtttggg ctcttttacg 480  
 230 gaggataata tcgtatccat gaggaaata gtcgcacgt ctggacttgg tgatgtctacg 540  
 231 tatttacctg aagctatccg tactatcccg gtcatcccg ctgtatcccg tgatggaaagc 600  
 232 gaagctgagt tgggtatgtt tgggtcgatt gatcaacttt tggagaagac aaaggtgaat 660  
 233 ccgaggatca tagggatctt ggttgttaat tgcacgtctt ttatccggc tccgtccctc 720  
 234 tcgtcgatga ttgttaccaa ctataactt cgtggaaaca ttataagcta caatctggc 780  
 235 ggaatgggtt cgactgttgg tttatattcg tcgtacttag ctaaaagact ttcggagaca 840  
 236 aatccaaaca cttagctttt agttatgagc actggaaaata tcacactaaa ctggatcatg 900  
 237 ggcaatgcacc ggtccaaact ctgtgtccat tttttttcc ggatgggggg agctcgccgtc 960  
 238 ttgttatcaa acaaaacccat tgataaaaaa agatcgaaat atcgttggt tactacttcg 1020  
 239 cgaaggccaca aagggtcgta ctgttatttc acatcgatca tatttcaaga aagaaactcc 1080  
 240 aacggcaaaa tcgggtgtaa cctctccaaa aatctaatgg cggtcgcagg ggacgcgttt 1140  
 241 aagactaaca tcacgcgtt tggccgttg gttttaccaa tgcggaaaca actttttttt 1200  
 242 ttccgcacgc tgggtgttcc aaaaattttcc aagaagaaaa ttacggccctaa catttccggac 1260  
 243 tttaaatctg cttttgcata tttctgttatt catcggtgtt gtcgagctgt ttggacgag 1320  
 244 cttggagaaga atttgcgtt gtcaagctgg catcttagagc cgtcgagaat gacgtttatc 1380  
 245 cggtttggta atacgtcgag tagtactttg tggtacgagc tggcgatattc ggaagccaaa 1440  
 246 gggaggatggaaaaggaga aagagtgttgg cagatgttgg gttgttccgttgg gtttaaatgt 1500  
 247 aataatgtctg tctggaaagc cttaaaagagc gttgtatccaa agaaagagaa caatccatgg 1560  
 248 atggatgaga tccaccagg tccgggttgc gttgttcaag gttgttggt gatgttttaat 1620  
 249 gttttgggtt gttgtatccgtt ctaatttggg agtgtaaagaa gtacttggt gctgtgttt 1680  
 W--> 250 caattactaa cttaaagagag tggtgttgcataa gcatagaaca aagtaantaa ctggaaatgt 1740  
 251 ctttttgggtt gttgtatccgtt cttcttattact gctgttgcataa gatgtttttt 1800  
 252 tttaaaaaa 1807  
 254 <210> SEQ ID NO: 5  
 255 <211> LENGTH: 505  
 256 <212> TYPE: PRT  
 257 <213> ORGANISM: Limnanthes douglasii  
 259 <220> FEATURE:

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260 <221> NAME/KEY: UNSURE  
 261 <222> LOCATION: (74) /  
 263 <220> FEATURE:  
 264 <221> NAME/KEY: UNSURE  
 265 <222> LOCATION: (77) /  
 267 <220> FEATURE:  
 268 <221> NAME/KEY: UNSURE  
 269 <222> LOCATION: (114) /  
 271 <400> SEQUENCE: 5  
 272 Met Ser Glu Thr Lys Pro Glu Lys Pro Leu Ile Ala Thr Val Lys Asn  
 273 1 5 10 15  
 275 Thr Leu Pro Asp Leu Lys Leu Ser Ile Asn Leu Lys His Val Lys Leu  
 276 20 25 30  
 278 Gly Tyr His Tyr Leu Ile Thr His Gly Met Tyr Leu Cys Leu Pro Pro  
 279 35 40 45  
 281 Leu Ala Leu Val Leu Phe Ala Gln Ile Ser Thr Leu Ser Leu Lys Asp  
 282 50 55 60  
 W--> 284 Phe Asn Asp Ile Trp Glu Gln Leu Gln Xaa Asn Leu Xaa Ser Val Val  
 285 65 70 75 80  
 287 Val Ser Ser Thr Leu Leu Val Ser Leu Leu Ile Leu Tyr Phe Met Thr  
 288 85 90 95  
 290 Arg Pro Arg Pro Val Tyr Leu Met Asp Phe Ala Cys Tyr Lys Pro Asp  
 291 100 105 110  
 W--> 293 Glu Xaa Arg Lys Ser Thr Arg Glu His Phe Met Lys Cys Gly Glu Ser  
 294 115 120 125  
 296 Leu Gly Ser Phe Thr Glu Asp Asn Ile Asp Phe Gln Arg Lys Leu Val  
 297 130 135 140  
 299 Ala Arg Ser Gly Leu Gly Asp Ala Thr Tyr Leu Pro Glu Ala Ile Gly  
 300 145 150 155 160  
 302 Thr Ile Pro Ala His Pro Ser Met Lys Ala Ala Arg Arg Glu Ala Glu  
 303 165 170 175  
 305 Leu Val Met Phe Gly Ala Ile Asp Gln Leu Leu Glu Lys Thr Lys Val  
 306 180 185 190  
 308 Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Cys Ser Leu Phe Ser  
 309 195 200 205  
 311 Pro Thr Pro Ser Leu Ser Ser Met Ile Val Asn His Tyr Lys Leu Arg  
 312 210 215 220  
 314 Gly Asn Ile Ile Ser Tyr Asn Leu Gly Gly Met Gly Cys Ser Ala Gly  
 315 225 230 235 240  
 317 Leu Ile Ser Val Asp Leu Ala Lys Arg Leu Leu Glu Thr Asn Pro Asn  
 318 245 250 255  
 320 Thr Tyr Ala Leu Val Met Ser Thr Glu Asn Ile Thr Leu Asn Trp Tyr  
 321 260 265 270  
 323 Met Gly Asn Asp Arg Ser Lys Leu Val Ser Asn Cys Leu Phe Arg Met  
 324 275 280 285  
 326 Gly Gly Ala Ala Val Leu Leu Ser Asn Lys Thr Ser Asp Lys Lys Arg  
 327 290 295 300  
 329 Ser Lys Tyr Gln Leu Val Thr Thr Val Arg Ser His Lys Gly Ala Asp  
 330 305 310 315 320

VERIFICATION SUMMARY  
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Input Set : A:\BB1117 US NA Seq Listing.txt  
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L:12 M:270 C: Current Application Number differs, Replaced Application Number  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:227 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4  
L:227 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4  
L:229 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4  
M:340 Repeated in SeqNo=4  
L:250 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4  
L:284 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5  
L:284 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5  
L:293 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5  
M:340 Repeated in SeqNo=5